

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/533,144B  
Source: IFW  
Date Processed by STIC: 2/8/07

# ENTERED



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/533,144B

DATE: 02/08/2007  
TIME: 11:07:57

Input Set : E:\seqlist.txt  
Output Set: N:\CRF4\02082007\J533144B.raw

4 <110> APPLICANT: MASUDA, ESTEBAN  
 6 <120> TITLE OF INVENTION: METHODS OF SCREENING CYCLIC PEPTIDES AND  
 7 IDENTIFYING TARGETS THEREFOR  
 10 <130> FILE REFERENCE: RIGL-023  
 12 <140> CURRENT APPLICATION NUMBER: 10/533,144B  
 13 <141> CURRENT FILING DATE: 2005-04-27  
 15 <150> PRIOR APPLICATION NUMBER: US03/27370  
 16 <151> PRIOR FILING DATE: 2003-08-30  
 18 <150> PRIOR APPLICATION NUMBER: 60/407,385  
 19 <151> PRIOR FILING DATE: 2002-08-30  
 21 <160> NUMBER OF SEQ ID NOS: 4  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1227  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: synthetic oligonucleotide  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: CDS  
 35 <222> LOCATION: (1)...(1227)  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: misc\_feature  
 39 <222> LOCATION: 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171  
 40 <223> OTHER INFORMATION: n = A,T,C or G  
 42 <400> SEQUENCE: 1  
 43 atg gag agc ggc agc ccc gag atc gag aag ctg agt cag agc gac atc 48  
 44 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile  
 45 1 5 10 15  
 47 tac tgg gac agc atg gtg agc atc acc gag acc ggc gtg gag gag gtg 96  
 48 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val  
 49 20 25 30  
 51 ttc gac ctg acc gtg ccc ggc ccc cac aac ttc gtg gcc aac gac atc 144  
 52 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile  
 53 35 40 45  
 W--> 55 atc gtc cac aac agc nnn nnn nnn tgc atc agc ggc gac agc ctg 192  
 W--> 56 Ile Val His Asn Ser Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu  
 57 50 55 60  
 59 atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg 240  
 60 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu  
 61 65 70 75 80  
 63 gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag 288  
 64 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys

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65	85	90	95	
67	cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta			336
68	Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu			
69	100	105	110	
71	gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc			384
72	Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala			
73	115	120	125	
75	aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta			432
76	Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu			
77	130	135	140	
79	agc cta aag gag cac atc gcc cta ccc cgg aag cta gag agc agc agc			480
80	Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser			
81	145	150	155	160
83	cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag			528
84	Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu			
85	165	170	175	
87	ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta			576
88	Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val			
89	180	185	190	
91	aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc			624
92	Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr			
93	195	200	205	
95	tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc			672
96	Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro			
97	210	215	220	
99	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc			720
100	Val Pro Trp Pro Thr Leu Val Thr Leu Thr His Gly Val Gln Cys			
101	225	230	235	240
103	ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc			768
104	Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser			
105	245	250	255	
107	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac			816
108	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
109	260	265	270	
111	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc			864
112	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr			
113	275	280	285	
115	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc			912
116	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly			
117	290	295	300	
119	aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg			960
120	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val			
121	305	310	315	320
123	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag			1008
124	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys			
125	325	330	335	
127	atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac			1056
128	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr			
129	340	345	350	

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131 cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac 1104  
 132 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 133 355 360 365  
 135 cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag 1152  
 136 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 137 370 375 380  
 139 cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act 1200  
 140 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 141 385 390 395 400  
 143 ctc ggc atg gac gag ctg tac aag taa 1227  
 144 Leu Gly Met Asp Glu Leu Tyr Lys \*  
 145 405  
 148 <210> SEQ ID NO: 2  
 149 <211> LENGTH: 408  
 150 <212> TYPE: PRT  
 151 <213> ORGANISM: Artificial Sequence  
 153 <220> FEATURE:  
 154 <221> NAME/KEY: VARIANT  
 155 <222> LOCATION: 54, 55, 56, 57  
 156 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
 158 <220> FEATURE:  
 159 <223> OTHER INFORMATION: synthetic polypeptide  
 161 <400> SEQUENCE: 2  
 162 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile  
 163 1 5 10 15  
 164 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val  
 165 20 25 30  
 166 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile  
 167 35 40 45  
 W--> 168 Ile Val His Asn Ser Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu  
 169 50 55 60  
 170 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu  
 171 65 70 75 80  
 172 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys  
 173 85 90 95  
 174 Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu  
 175 100 105 110  
 176 Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala  
 177 115 120 125  
 178 Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu  
 179 130 135 140  
 180 Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser  
 181 145 150 155 160  
 182 Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu  
 183 165 170 175  
 184 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val  
 185 180 185 190  
 186 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr  
 187 195 200 205

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188 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 189 210 215 220  
 190 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys  
 191 225 230 235 240  
 192 Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser  
 193 245 250 255  
 194 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 195 260 265 270  
 196 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 197 275 280 285  
 198 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 199 290 295 300  
 200 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val  
 201 305 310 315 320  
 202 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 203 325 330 335  
 204 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 205 340 345 350  
 206 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 207 355 360 365  
 208 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 209 370 375 380  
 210 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 211 385 390 395 400  
 212 Leu Gly Met Asp Glu Leu Tyr Lys  
 213 405  
 216 <210> SEQ ID NO: 3  
 217 <211> LENGTH: 5  
 218 <212> TYPE: PRT  
 219 <213> ORGANISM: Artificial Sequence  
 221 <220> FEATURE:  
 222 <223> OTHER INFORMATION: synthetic peptide  
 224 <400> SEQUENCE: 3  
 225 Gly Ser Gly Gly Ser  
 226 1 5  
 229 <210> SEQ ID NO: 4  
 230 <211> LENGTH: 4  
 231 <212> TYPE: PRT  
 232 <213> ORGANISM: Artificial Sequence  
 234 <220> FEATURE:  
 235 <223> OTHER INFORMATION: synthetic peptide  
 237 <400> SEQUENCE: 4  
 238 Ala Gly Pro Ile  
 239 1

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/533,144B

DATE: 02/08/2007  
TIME: 11:07:58

Input Set : E:\seqlist.txt  
Output Set: N:\CRF4\02082007\J533144B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 160,161,162,163,164,165,166,167,168,169,170,171/  
Seq#:1; Xaa Pos. 54,55,56,57  
Seq#:2; Xaa Pos. 54,55,56,57

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/533,144B

DATE: 02/08/2007

TIME: 11:07:58

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\02082007\J533144B.raw

L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:144

L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:192

L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:48